In the Claims:

Please cancel claims 24-38 and 81 without prejudice to future prosecution thereof.

Please amend claims 41, 42, 48, 49, 51, 54-57, 59, 60, 67, 69, 70, 72, 73, 79, 80, 91 and 96 as follows:

I1

41. (Amended) A kit for amplifying and detecting *Mycobacterial* nucleic acid, containing a first oligonucleotide of about 24 to about 100 bases in length comprising a nucleotide base sequence GTCTTGTGGTGGAAAGCGCTTTAG (SEQ ID: 3) and [at least one additional] one or more of second oligonucleotides of about 23 to about 100 bases in length selected from the group consisting of xGCCGGTCACCCCACCAACAAGCT (SEQ ID: 1) and xGGATAAGCCTGGGAAACTGGGTCTAATACC (SEQ ID: 2), wherein x is nothing or is a sequence recognized by an RNA polymerase.

42. (Amended) A kit for amplifying and detecting *Mycobacterial* nucleic acid, containing a first oligonucleotide of about 23 to about 100 bases in length comprising a nucleotide base sequence GGAGGATATGTCTCAGCGCTACC (SEQ ID: 8) and [at least one additional] one or more of second oligonucleotides of about 20 to about 100 bases in length selected from the group consisting of xCCAGGCCACTTCCGCTAACC (SEQ ID: 6) and xCGCGGAACAGGCTAAACCGCACGC (SEQ ID: 7), wherein x is nothing or is a sequence recognized by an RNA polymerase.

I2

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48. (Amended) The kit of claim 41, wherein one or more of said second oligonucleotides is modified at 3' end to reduce or block extension of said one or more of said second oligonucleotides by a polymerase [sequences has a 3' end modified to reduce or block extension by a polymerase].

49. (Amended) The kit of claim [41] 48, wherein one or more of said second oligonucleotides is unmodified at 3' end [at least one said oligonucleotide comprises a mixture comprising modified and unmodified members comprising a common nucleotide sequence].

51. (Amended) A plurality of [The] oligonucleotides of claim 40, wherein one or more of said oligonucleotides is unmodified at 3' end and one or more of said oligonucleotides is modified at 3' end to reduce or block extension by a polymerase [comprising a mixture comprising members selected from the group consisting of

a) 3' unmodified members and members modified at their 3' end to reduce or block extension by a polymerase, and

b) a mixture of members differently modified at their 3' ends to reduce or block extension by a polymerase].

54. (Amended) The plurality of oligonucleotides of claim 51, wherein one or more of said oligonucleotides is differently modified at 3' end to reduce or block extension by a polymerase [The composition of claim 27 comprising a reverse transcriptase which is both said DNA-dependent DNA polymerase and said RNA-dependent DNA polymerase].

55. (Amended) The kit of claim 42, wherein one or more of said second oligonucleotides is modified at 3' end to reduce or block extension of said one or more of said second oligonucleotides by a polymerase [sequences has a 3' end modified to reduce or block extension by a polymerase].

56. (Amended) The kit of claim [42] 55, wherein one or more of said second oligonucleotides is unmodified at 3' end [comprising a mixture comprising unmodified members and members modified at their 3' end to reduce or block extension of said members by a

polymerase, wherein said members comprise one or more of said sequences].

57. (Amended) A nucleic acid hybridization probe, comprising an oligonucleotide from 10 to 100 nucleotides in length which will hybridize with at least 10 contiguous bases of a nucleotide base sequence region of *Mycobacterium tuberculosis* nucleic acid to form a detectable hybridization duplex under selective hybridization conditions, wherein said region consists of a nucleotide base sequence selected from the group consisting of SEQ ID NO[s.]: 3, [and] SEQ ID NO: 8, and their fully complementary sequences of the same length.

59. (Amended) The probe of claim 57, wherein said oligonucleotide comprises a nucleotide base sequence selected from the group consisting of SEQ ID NO[s.]: 3, [and] SEQ ID NO: 8, and their fully complementary sequences of the same length.

60. (Amended) The probe of claim 57, wherein said oligonucleotide consists of a nucleotide base sequence selected from the group consisting of SEQ ID NO[s.]: 3, [and] SEQ ID NO: 8, and their fully complementary sequences of the same length.

67. (Amended) An oligonucleotide from 10 to 100 nucleotides in length able to bind to or extend through a region of *Mycobacterium tuberculosis* nucleic acid, wherein said region consists of a nucleotide base sequence selected from the group consisting of SEQ ID NO[s.]: 2, SEQ ID NO: 7, SEQ ID NO: 22 and SEQ ID NO: 23, and their fully complementary sequences of the same length.

69. (Amended) The oligonucleotide of claim 67, comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO[s.]: 2, SEQ ID NO: 7, SEQ ID NO: 22 and SEQ ID NO: 23, and their fully complementary sequences of the same length.

Sub K2 Cancel

70. (Amended) The oligonucleotide of claim 67, consisting of a nucleotide base sequence selected from the group consisting of SEQ ID NO[s.]: 2, SEQ ID NO: 7, SEQ ID NO: 22 and SEQ ID NO: 23, and their fully complementary sequences of the same length.

I10 Sub M8

72. (Amended) The oligonucleotide of claim 71, comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO[s.]: 1, SEQ ID NO: 6 and SEQ ID NO: 19.

73. (Amended) The oligonucleotide of claim 71, consisting of a sequence selected from the group consisting of SEQ ID NO[s.]: 1, SEQ ID NO: 6 and SEQ ID NO: 19.

I11 Sub M10

79. (Amended) The composition of any one of claims 74, 76, or 77, further comprising a nucleic acid hybridization assay probe from about 10 to about 100 nucleotide bases in length which will hybridize with at least 10 contiguous bases of a nucleotide base sequence region of *Mycobacterium tuberculosis* nucleic acid to form a detectable duplex under hybridization conditions; wherein said region is selected from the group consisting of SEQ ID NO: 8 [or] and the perfectly complementary sequence thereto.

Sub M11

80. (Amended) The composition of claim 79, wherein said probe comprises an oligonucleotide [with a nucleotide base sequence comprising] selected from the group consisting of SEQ ID NO: 8 [or] and the perfectly complementary sequence thereto.

I12

91. (Amended) The composition of claim 89, wherein said probe comprises an oligonucleotide [with a nucleotide base sequence] selected from the group consisting of SEQ ID NO: 3 [or] and the perfectly complementary sequence thereto.

I13 Sub M9

96. (Amended) A probe mix comprising:

I 13 Conclude

a nucleic acid hybridization assay probe comprising an oligonucleotide from 10 to 100 nucleotides in length which will hybridize with at least 10 contiguous bases of a region of *Mycobacterium tuberculosis* nucleic acid to form a detectable hybridization duplex under selective hybridization conditions, wherein said region is selected from the group consist[s]ing of SEQ ID NO. 8[, or] and its fully complementary sequence of the same length, and a helper probe.

Please and add new claims 102-142 as follows:

I 14

SUB M22

102. A composition comprising:

a nucleic acid comprising a (+) target sequence,

a first oligonucleotide comprising a primer sequence able to hybridize at or near the 3'-end of said (+) target sequence, a 5' promoter sequence, and a modification at or near the 3' end of said first oligonucleotide primer sequence which reduces or blocks extension of said first oligonucleotide primer sequence by a polymerase compared to said first oligonucleotide primer sequence not having said modification,

a second oligonucleotide comprising a primer sequence able to hybridize at or near said 3'-end of said (+) target sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said second oligonucleotide primer sequence which reduces or blocks extension of said second oligonucleotide primer sequence by a polymerase compared to said second oligonucleotide primer sequence not having said modification, wherein said second oligonucleotide hybridizes to said (+) target sequence in effectively the same position as said first oligonucleotide and said second oligonucleotide modification, if present, is different than said first oligonucleotide modification,

a third oligonucleotide comprising a primer sequence able to hybridize to the 3'-end of a (-) target nucleic acid sequence which is produced during said method and which is the complement of said (+) target sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end of said third oligonucleotide primer sequence able to reduce or block extension of said third oligonucleotide primer sequence by a

polymerase compared to said third oligonucleotide primer sequence not having said modification,

an enzyme selected from the group consisting of DNA dependent DNA polymerase and RNA dependent DNA polymerase, and

one or more RNA polymerases that recognize said first and said second oligonucleotide 5' promoter sequences.

103. The composition of claim 102, wherein said (+) target sequence is RNA.

104. The composition of claim 102, wherein said composition further comprises RNAse H activity.

105. The composition of claim 104, wherein said RNAse H activity is supplied by an exogenous RNAse H from *E. coli*.

106. The composition of claim 104, wherein said RNAse H activity is supplied by a reverse transcriptase.

107. The composition of claim 102, wherein said enzyme is a reverse transcriptase which is both a DNA-dependent DNA polymerase and an RNA-dependent DNA polymerase.

108. The composition of claim 102, further comprising a molecule selected from the group consisting of DMSO, dimethylformamide, ethylene glycol, zinc and glycerol.

109. The composition of claim 102, further comprising a helper oligonucleotide.

110. The composition of claim 102, wherein said first and said second oligonucleotides are present in a molar ratio of between 1:1 and 1000:1.

111. The composition of claim 102, wherein said second oligonucleotide contains said modification.

SUB M24

I 14 Cont.

112. The composition of claim 111, further comprising a fourth oligonucleotide comprising a primer sequence that hybridizes in effectively the same position as said first and second oligonucleotides and an optionally present 5' promoter sequence, wherein said fourth oligonucleotide does not contain a modification at or near its 3' end to reduce or block primer extension of said fourth oligonucleotide primer sequence.

113. The composition of claim 102, wherein said first oligonucleotide modification and said second oligonucleotide modification are each independently selected from the group consisting of alkane diol modification, 3' deoxynucleotide residue, nucleotide with a nonphosphodiester linkage, non-nucleotide modification, base non-complementary to said (+) target sequence, and dideoxynucleotide.

114. The composition of claim 102, wherein said first oligonucleotide modification and said second oligonucleotide modification are each independently selected from the group consisting of cordycepin, ribonucleotide, and phosphorothioate nucleotide.

115. The composition of claim 102, wherein said third oligonucleotide does not contain said modification.

116. The composition of claim 102, wherein said third oligonucleotide contains said 5' promoter sequence.

117. The composition of claim 116, wherein said third oligonucleotide contains said modification.

118. The composition of claim 102, wherein said first and said second oligonucleotide primer sequences are the same.

119. The composition of claim 102, wherein said first and said second oligonucleotide primer sequences are different.

120. A composition comprising:

a nucleic acid comprising a (+) target sequence,

a first oligonucleotide comprising a primer sequence able to hybridize to the 3'-end of said (+) target sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end of said first oligonucleotide primer sequence able to reduce or block extension of said first oligonucleotide primer sequence by a polymerase compared to said first oligonucleotide primer sequence not having said modification,

a second oligonucleotide comprising a primer sequence able to hybridize at or near the 3'-end of a (-) target nucleic acid sequence which is produced during said method and which is the complement of said (+) target sequence, a 5' promoter sequence, and a modification at or near the 3' end of said second oligonucleotide primer sequence which reduces or blocks extension of said second oligonucleotide primer sequence by a polymerase compared to said second oligonucleotide primer sequence not having said modification,

a third oligonucleotide comprising a primer sequence able to hybridize at or near said 3'-end of said (-) target sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said third oligonucleotide primer sequence which reduces or blocks extension of said third oligonucleotide primer sequence by a polymerase compared to said third oligonucleotide primer sequence not having said modification, wherein said third oligonucleotide hybridizes to said (-) target sequence in effectively the same position as said second oligonucleotide and said third oligonucleotide modification, if present, is different than said second oligonucleotide modification,

an enzyme selected from the group consisting of DNA dependent DNA polymerase and RNA dependent DNA polymerase, and

one or more RNA polymerases that recognize said first and said second oligonucleotide 5' promoter sequences.

121. The composition of claim 120, wherein said (+) target sequence is RNA.

122. The composition of claim 120, wherein said composition further comprises RNAse H activity.

123. The composition of claim 122, wherein said RNAse H activity is supplied by an exogenous RNAse H from *E. coli*.

124. The composition of claim 122, wherein said RNAse H activity is supplied by a reverse transcriptase.

125. The composition of claim 120, wherein said enzyme is a reverse transcriptase which is both a DNA-dependent DNA polymerase and an RNA-dependent DNA polymerase.

126. The composition of claim 120, further comprising a molecule selected from the group consisting of DMSO, dimethylformamide, ethylene glycol, zinc and glycerol.

127. The composition of claim 120, further comprising a helper oligonucleotide.

128. The composition of claim 120, wherein said second and said third oligonucleotides are present in a molar ratio of between 1:1 and 1000:1.

129. The composition of claim 120, wherein said third oligonucleotide contains said

modification.

130. The composition of claim 129, further comprising a fourth oligonucleotide comprising a primer sequence that hybridizes in effectively the same position as said second and third oligonucleotides and an optionally present 5' promoter sequence, wherein said fourth oligonucleotide does not contain a modification at or near its 3' end to reduce or block primer extension of said fourth oligonucleotide primer sequence.

131. The composition of claim 120, wherein said second oligonucleotide modification and said third oligonucleotide modification are each independently selected from the group consisting of alkane diol modification, 3' deoxynucleotide residue, nucleotide with a nonphosphodiester linkage, non-nucleotide modification, base non-complementary to said (+) target sequence, and dideoxynucleotide.

132. The composition of claim 120, wherein said first oligonucleotide modification and said second oligonucleotide modification are each independently selected from the group consisting of cordycepin, ribonucleotide, and phosphorothioate nucleotide.

133. The composition of claim 120, wherein said first oligonucleotide does not contain said modification.

134. The composition of claim 120, wherein said first oligonucleotide contains said 5' promoter sequence.

135. The composition of claim 120, wherein said third oligonucleotide contains said modification.

136. The composition of claim 134, wherein said first oligonucleotide 5' promoter

sequence, said second oligonucleotide 5' promoter sequence and said third oligonucleotide 5' promoter sequence are the same.

137. The composition of claim 120, wherein said second and said third oligonucleotide primer sequences are the same.

138. The composition of claim 120, wherein said second and said third oligonucleotide primer sequences are different.

139. A kit comprising:

a first oligonucleotide comprising a primer sequence able to hybridize at or near the 3'-end of a (+) target sequence, a 5' promoter sequence, and a modification at or near the 3' end of said first oligonucleotide primer sequence which reduces or blocks extension of said first oligonucleotide primer sequence by a polymerase compared to said first oligonucleotide primer sequence not having said modification,

a second oligonucleotide comprising a primer sequence able to hybridize at or near said 3'-end of said (+) target sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said second oligonucleotide primer sequence which reduces or blocks extension of said second oligonucleotide primer sequence by a polymerase compared to said second oligonucleotide primer sequence not having said modification, wherein said second oligonucleotide hybridizes to said (+) target sequence in effectively the same position as said first oligonucleotide and said second oligonucleotide modification, if present, is different than said first oligonucleotide modification,

a third oligonucleotide comprising a primer sequence able to hybridize to the 3'-end of a (-) target nucleic acid sequence which is produced during said method and which is the complement of said (+) target sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end of said third oligonucleotide primer sequence able to reduce or block extension of said third oligonucleotide primer sequence by a

polymerase compared to said third oligonucleotide primer sequence not having said modification,

an enzyme selected from the group consisting of DNA dependent DNA polymerase and RNA dependent DNA polymerase, and

one or more RNA polymerases that recognize said first and said second oligonucleotide 5' promoter sequences.

140. The kit of claim 139, further comprising a probe able to indicate the presence of said (+) target sequence or said (-) target sequence.

141. A kit comprising:

a first oligonucleotide comprising a primer sequence able to hybridize to the 3'-end of a (+) target sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end of said first oligonucleotide primer sequence able to reduce or block extension of said first oligonucleotide primer sequence by a polymerase compared to said first oligonucleotide primer sequence not having said modification,

a second oligonucleotide comprising a primer sequence able to hybridize at or near the 3'-end of a (-) target nucleic acid sequence which is produced during said method and which is the complement of said (+) target sequence, a 5' promoter sequence, and a modification at or near the 3' end of said second oligonucleotide primer sequence which reduces or blocks extension of said second oligonucleotide primer sequence by a polymerase compared to said second oligonucleotide primer sequence not having said modification,

a third oligonucleotide comprising a primer sequence able to hybridize at or near said 3'-end of said (-) target sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said third oligonucleotide primer sequence which reduces or blocks extension of said third oligonucleotide primer sequence by a polymerase compared to said third oligonucleotide primer sequence not having said modification, wherein said third oligonucleotide hybridizes to said (-) target sequence in effectively the same position as said